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## SEQUENCE LISTING

<110> LEUNG, DAVID W.  
 ADOUREL, DANIEL  
 HOLLENBACK, DAVID

<120> MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE

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<140> 09/970,989

<141> 2001-10-05

<150> 09/215,252

<151> 1998-12-18

<150> 08/618,651

<151> 1996-03-19

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Lys His Val Ala Thr Phe Gly His Met Phe Gly Arg Leu Phe Thr Ala  
35 40 45

Pro Leu Phe Gly Leu Lys Val Glu Cys Arg Lys Pro Ala Asp Ala Glu  
50 55 60

Asn Tyr Gly Asn Ala Ile Tyr Ile Ala Asn His Gln Asn Asn Tyr Asp  
65 70 75 80

Met Val Thr Ala Ala Asn Ile Val Gln Pro Pro Thr Val Thr Val Gly  
85 90 95

Lys Lys Ser Leu Leu Trp Ile Pro Phe Phe Phe Thr Gly Gln Leu Tyr  
100 105 110

Trp Leu Thr Gly Asn Leu Leu Ile Asp Arg Asn Asn Arg Ala Lys Ala  
115 120 125

His Ser Thr Ile Ala Ala Val Val Asn His Phe Lys Lys Arg Arg Ile  
130 135 140

Ser Ile Trp Met Phe Pro Glu Gly Thr Arg Ser Arg Gly Arg Gly Leu  
145 150 155 160

Leu Pro Phe Lys Thr Gly Ala Phe Thr Phe His Ala Ala Ile Ala Ala  
165 170 175

Gly Val Pro Ile Ile Pro Val Cys Val Ser Asn Thr Ser Asn Lys Val  
180 185 190

Asn Leu Asn Arg Leu Asn Asn Gly Leu Val Ile Val Glu Met Leu Pro  
195 200 205

Pro Val Asp Val Ser Glu Tyr Gly Lys Asp Gln Val Arg Glu Leu Ala  
210 215 220

Ala His Cys Arg Phe Thr Ala Leu Met Glu Gln Lys Ile Ala Glu Leu  
225 230 235 240

Asp Lys Glu Val Ala Glu Arg Glu Ala Thr Gly Lys Val  
245 250

<210> 10  
 <211> 289  
 <212> PRT  
 <213> *Lupinus douglassi*

<400> 10

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Pro	Ala	Val	Ala	Ala	Thr	Ala	Asp	Asp	Asp	Lys	Asp	Gly	Val	Phe	Met
			20				25						30		
Val	Leu	Leu	Ser	Cys	Phe	Lys	Ile	Phe	Val	Cys	Phe	Ala	Phe	Thr	Val
		35					40					45			
Val	Leu	Ile	Thr	Ala	Val	Ala	Trp	Gly	Leu	Ile	Met	Val	Leu	Leu	Leu
	50					55					60				
Pro	Trp	Pro	Tyr	Met	Arg	Ile	Arg	Leu	Gly	Asn	Leu	Tyr	Gly	His	Ile
	65				70					75					80
Ile	Gly	Gly	Leu	Val	Ile	Trp	Ile	Tyr	Gly	Ile	Pro	Ile	Lys	Ile	Gln
				85					90					95	
Gly	Ser	Glu	His	Thr	Lys	Lys	Arg	Ala	Ile	Phe	Thr	Tyr	Ile	Ser	Asn
			100					105					110		
His	Ala	Ser	Pro	Ile	Asp	Ala	Phe	Phe	Val	Met	Trp	Leu	Ala	Pro	Ile
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Gly	Thr	Val	Gly	Val	Ala	Lys	Lys	Glu	Val	Ile	Trp	Tyr	Pro	Leu	Leu
	130					135					140				
Gly	Gln	Leu	Tyr	Thr	Leu	Ala	His	His	Ile	Arg	Ile	Asp	Arg	Ser	Asn
	145				150					155					160
Pro	Ala	Ala	Ala	Ile	Gln	Ser	Phe	Thr	Met	Lys	Glu	Ala	Val	Arg	Val
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Ile	Thr	Glu	Lys	Asn	Leu	Ser	Leu	Ile	Met	Phe	Pro	Glu	Gly	Thr	Arg
			180					185					190		
Ser	Gly	Asp	Gly	Arg	Leu	Leu	Pro	Phe	Lys	Lys	Gly	Phe	Val	His	Leu
		195					200					205			
Ala	Leu	Gln	Ser	His	Leu	Pro	Ile	Val	Pro	Met	Ile	Leu	Thr	Gly	Thr
	210					215					220				
His	Leu	Ala	Trp	Phe	Thr	Arg	Lys	Gly	Thr	Phe	Arg	Val	Arg	Pro	Val
	225				230					235					240
Pro	Ile	Thr	Val	Lys	Tyr	Leu	Pro	Pro	Ile	Asn	Thr	Asp	Asp	Trp	Thr
				245					250					255	
Val	Asp	Lys	Ile	Asp	Asp	Tyr	Val	Lys	Met	Ile	His	Asp	Ile	Tyr	Val
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Lys

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 <212> PRT  
 <213> Cocos nucifera

<400> 11

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 Gly Gln Pro Ser Arg Arg Pro Ala Asp Ala Asp Asp Phe Phe Thr Val  
 35 40 45  
 Asp Asp Asp Arg Trp Ile Thr Val Ile Leu Ser Val Val Arg Ile Ala  
 50 55 60  
 Ala Cys Phe Leu Ser Met Met Val Thr Thr Ile Val Trp Asn Met Ile  
 65 70 75 80  
 Met Leu Ile Leu Leu Pro Trp Pro Tyr Ala Arg Ile Arg Gln Gly Asn  
 85 90 95  
 Leu Tyr Gly His Val Thr Gly Arg Met Leu Phe Thr Met Trp Ile Leu  
 100 105 110  
 Gly Asn Pro Ile Thr Ile Glu Gly Ser Glu Phe Ser Asn Thr Arg Ala  
 115 120 125  
 Ile Tyr Ile Cys Asn His Ala Ser Leu Val Asp Ile Phe Leu Ile Met  
 130 135 140  
 Trp Leu Ile Pro Lys Gly Thr Val Thr Ile Ala Lys Lys Glu Ile Ile  
 145 150 155 160  
 Trp Tyr Pro Leu Phe Gly Gln Phe Thr Leu Tyr Val Leu Ala Asn His  
 165 170 175  
 Gln Arg Ile Asp Arg Ser Asn Pro Ser Ala Ala Ile Glu Ser Ile Lys  
 180 185 190  
 Glu Val Ala Arg Ala Val Val Lys Lys Asn Leu Ser Leu Ile Ile Phe  
 195 200 205  
 Pro Glu Gly Thr Arg Ser Lys Thr Gly Arg Leu Leu Pro Phe Lys Lys  
 210 215 220  
 Gly Phe Ile His Phe Thr Ile Ala Leu Gln Thr Arg Leu Pro Ile Val  
 225 230 235 240

[illegible]



cac aac ttc gag atc gac ttc ctc tgt ggg tgg acc atg tgt gag cgc	516
His Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys Glu Arg	
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ttc gga gtg ctg ggg agc tcc aag gtc ctc gct aag aag gag ctg ctc	564
Phe Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys Glu Leu Leu	
115 120 125	
tac gtg ccc ctc atc ggc tgg acg tgg tac ttt ctg gag att gtg ttc	612
Tyr Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu Glu Ile Val Phe	
130 135 140	
tgc aag cgg aag tgg gag gag gac cgg gac acc gtg gtc gaa ggg ctg	660
Cys Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr Val Val Glu Gly Leu	
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Arg Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys	
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gag ggg acg cgc ttc acg gag acc aag cac cgc gtt agc atg gag gtg	756
Glu Gly Thr Arg Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val	
180 185 190	
gcg gct gct aag ggg ctt cct gtc ctc aag tac cac ctg ctg ccg cgg	804
Ala Ala Ala Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg	
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acc aag ggc ttc acc acc gca gtc aag tgc ctc cgg ggg aca gtc gca	852
Thr Lys Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala	
210 215 220	
gct gtc tat gat gta acc ctg aac ttc aga gga aac aag aac ccg tcc	900
Ala Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser	
225 230 235	
ctg ctg ggg atc ctc tac ggg aag aag tac gag gcg gac atg tgc gtg	948
Leu Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val	
240 245 250 255	
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Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala	
260 265 270	
cag tgg ctt cat aaa ctg tac cag gag aag gac gcg ctc cag gag ata	1044
Gln Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile	
275 280 285	
tat aat cag aag ggc atg ttt cca ggg gag cag ttt aag cct gcc cgg	1092
Tyr Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg	
290 295 300	
agg ccg tgg acc ctc ctg aac ttc ctg tcc tgg gcc acc att ctc ctg	1140
Arg Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu	
305 310 315	

tct ccc ctc ttc agt ttt gtc ttg ggc gtc ttt gcc agc gga tca cct 1188  
 Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser Pro  
 320 325 330 335

ctc ctg atc ctg act ttc ttg ggg ttt gtg gga gca gct tcc ttt gga 1236  
 Leu Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser Phe Gly  
 340 345 350

gtt cgc aga ctg ata gga gta act gag ata gaa aaa ggc tcc agc tac 1284  
 Val Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly Ser Ser Tyr  
 355 360 365

gga aac caa gag ttt aag aaa aag gaa taattaatgg ctgtgactga 1331  
 Gly Asn Gln Glu Phe Lys Lys Lys Glu  
 370 375

acacacgcgg ccctgacggt ggtatccagt taactcaaaa ccaacacaca gagtgcagga 1391

aaagacaatt agaaactatt tttcttatta actgggtgact aatattaaca aaacttgagc 1451

caagagtaaa gaattcagaa ggctgtcag gtgaagtctt cagcctccca cagcgcaggg 1511

tcccagcatc tccacgcgcg cccgtgggag gtgggtccgg ccggagagggc ctcccgcgga 1571

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<210> 13

<211> 376

<212> PRT

<213> Homo sapiens

<400> 13

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Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu Tyr Arg Arg  
 35 40 45

Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln Leu Val Met Leu  
 50 55 60

Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln Ala  
 65 70 75 80

Thr Val Glu Arg Phe Gly Lys Glu His Ala Val Ile Ile Leu Asn His  
 85 90 95

Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys Glu Arg Phe  
 100 105 110

Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys Glu Leu Leu Tyr  
 115 120 125

Val	Pro	Leu	Ile	Gly	Trp	Thr	Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys
130						135					140				
Lys	Arg	Lys	Trp	Glu	Glu	Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg
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Arg	Leu	Ser	Asp	Tyr	Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu
			165						170					175	
Gly	Thr	Arg	Phe	Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala
			180					185					190		
Ala	Ala	Lys	Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr
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Lys	Gly	Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala
210						215					220				
Val	Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu
225					230					235					240
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val	Arg
			245						250					255	
Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala	Ala	Gln
			260					265					270		
Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln	Glu	Ile	Tyr
		275					280					285			
Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys	Pro	Ala	Arg	Arg
290						295					300				
Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala	Thr	Ile	Leu	Leu	Ser
305					310					315					320
Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe	Ala	Ser	Gly	Ser	Pro	Leu
			325						330					335	
Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val	Gly	Ala	Ala	Ser	Phe	Gly	Val
			340					345					350		
Arg	Arg	Leu	Ile	Gly	Val	Thr	Glu	Ile	Glu	Lys	Gly	Ser	Ser	Tyr	Gly
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 taattatgcg gcaaccatac agggaccctc tgcggccatc atggagagcc ttcattctgc 180  
 ccgtacagtt ttaagcgaaa aaggaagtat acaacaaagt ccataactgg tc atg ctg 238  
 Met Leu

1

ctg gag tgg tgg tcc tgc acg gag tgt aca ctg ttc acg gac cag gcc 286  
 Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu Phe Thr Asp Gln Ala  
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acg gta gag cgc ttt ggg aag gag cac gca gtc atc atc ctc aac cac 334  
 Thr Val Glu Arg Phe Gly Lys Glu His Ala Val Ile Ile Leu Asn His  
 20 25 30

aac ttc gag atc gac ttc ctc tgt ggg tgg acc atg tgt gag cgc ttc 382  
 Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys Glu Arg Phe  
 35 40 45 50

gga gtg ctg ggg agc tcc aag gtc ctc gct aag aag gag ctg ctc tac 430  
 Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys Glu Leu Leu Tyr  
 55 60 65

gtg ccc ctc atc ggc tgg acg tgg tac ttt ctg gag att gtg ttc tgc 478  
 Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu Glu Ile Val Phe Cys  
 70 75 80

aag cgg aag tgg gag gag gac cgg gac acc gtg gtc gaa ggg ctg agg 526  
 Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr Val Val Glu Gly Leu Arg  
 85 90 95

cgc ctg tgc gac tac ccc gag tac atg tgg ttt ctc ctg tac tgc gag 574  
 Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu  
 100 105 110

ggg acg cgc ttc acg gag acc aag cac cgc gtt agc atg gag gtg gcg 622  
 Gly Thr Arg Phe Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala  
 115 120 125 130

gct gct aag ggg ctt cct gtc ctc aag tac cac ctg ctg ccg cgg acc 670  
 Ala Ala Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr  
 135 140 145

aag ggc ttc acc acc gca gtc aag tgc ctc cgg ggg aca gtc gca gct 718  
 Lys Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala  
 150 155 160

gtc tat gat gta acc ctg aac ttc aga gga aac aag aac ccg tcc ctg 766  
 Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu  
 165 170 175

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ctg ggg atc ctc tac ggg aag aag tac gag gcg gac atg tgc gtg agg 814
Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val Arg
180 185 190

aga ttt cct ctg gaa gac atc ccg ctg gat gaa aag gaa gca gct cag 862
Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala Ala Gln
195 200 205 210

tgg ctt cat aaa ctg tac cag gag aag gac gcg ctc cag gag ata tat 910
Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu Ile Tyr
215 220 225

aat cag aag ggc atg ttt cca ggg gag cag ttt aag cct gcc cgg agg 958
Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala Arg Arg
230 235 240

ccg tgg acc ctc ctg aac ttc ctg tcc tgg gcc acc att ctc ctg tct 1006
Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu Leu Ser
245 250 255

ccc ctc ttc agt ttt gtc ttg ggc gtc ttt gcc agc gga tca cct ctc 1054
Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser Pro Leu
260 265 270

ctg atc ctg act ttc ttg ggg ttt gtg gga gca gct tcc ttt gga gtt 1102
Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser Phe Gly Val
275 280 285 290

cgc aga ctg ata gga gta act gag ata gaa aaa ggc tcc agc tac gga 1150
Arg Arg Leu Ile Gly Val Thr Glu Ile Glu Lys Gly Ser Ser Tyr Gly
295 300 305

aac caa gag ttt aag aaa aag gaa taattaatgg ctgtgactga acacacgcgg 1204
Asn Gln Glu Phe Lys Lys Lys Glu
310

ccctgacggg ggtatccagt taactcaaaa ccaacacaca gagtgcagga aaagacaatt 1264

agaaactatt tttcttatta actggtgact aatattaaca aaacttgagc caagagtaaa 1324

gaattcagaa ggcctgtcag gtgaagtctt cagcctccca cagcgcaggg tcccagcatc 1384

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ttttaaaaaa aaaaaaaaaa 1523

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&lt;210&gt; 15

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 15

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 Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly Trp Thr Met Cys Glu  
 35 40 45  
 Arg Phe Gly Val Leu Gly Ser Ser Lys Val Leu Ala Lys Lys Glu Leu  
 50 55 60  
 Leu Tyr Val Pro Leu Ile Gly Trp Thr Trp Tyr Phe Leu Glu Ile Val  
 65 70 75 80  
 Phe Cys Lys Arg Lys Trp Glu Glu Asp Arg Asp Thr Val Val Glu Gly  
 85 90 95  
 Leu Arg Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu Tyr  
 100 105 110  
 Cys Glu Gly Thr Arg Phe Thr Glu Thr Lys His Arg Val Ser Met Glu  
 115 120 125  
 Val Ala Ala Ala Lys Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro  
 130 135 140  
 Arg Thr Lys Gly Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val  
 145 150 155 160  
 Ala Ala Val Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro  
 165 170 175  
 Ser Leu Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys  
 180 185 190  
 Val Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala  
 195 200 205  
 Ala Gln Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln Glu  
 210 215 220  
 Ile Tyr Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys Pro Ala  
 225 230 235 240  
 Arg Arg Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala Thr Ile Leu  
 245 250 255  
 Leu Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe Ala Ser Gly Ser  
 260 265 270  
 Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val Gly Ala Ala Ser Phe  
 275 280 285  
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ctg	aag	tct	cag	ttc	ctg	tgc	cac	ctg	gtc	ttc	tgc	tac	gtc	ttt	att		223					
Leu	Lys	Ser	Gln	Phe	Leu	Cys	His	Leu	Val	Phe	Cys	Tyr	Val	Phe	Ile							
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gcc tca ggg cta atc atc aac acc att cag ctc ttc act ctc ctc ctc 271																						
Ala	Ser	Gly	Leu	Ile	Ile	Asn	Thr	Ile	Gln	Leu	Phe	Thr	Leu	Leu	Leu							
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tgg ccc att aac aag cag ctc ttc cgg aag atc aac tgc aga ctg tcc 319																						
Trp	Pro	Ile	Asn	Lys	Gln	Leu	Phe	Arg	Lys	Ile	Asn	Cys	Arg	Leu	Ser							
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tat tgc atc tca agc cag ctg gtg atg ctg ctg gag tgg tgg tgg ggc 367																						
Tyr	Cys	Ile	Ser	Ser	Gln	Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Gly							
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acg gaa tgc acc atc ttc acg gac cgg cgc gcc tac ctc aag tat ggg 415																						
Thr	Glu	Cys	Thr	Ile	Phe	Thr	Asp	Pro	Arg	Ala	Tyr	Leu	Lys	Tyr	Gly							
															75			80		85		
aag gaa aat gcc atc gtg gtt ctc aac cac aag ttt gaa att gac ttt 463																						
Lys	Glu	Asn	Ala	Ile	Val	Val	Leu	Asn	His	Lys	Phe	Glu	Ile	Asp	Phe							
															90			95		100		
ctg tgt ggc tgg agc ctg tcc gaa cgc ttt ggg ctg tta ggg ggc tcc 511																						
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aag gtc ctg gcc aag aaa gag ctg gcc tat gtc cca att atc ggc tgg 559																						
Lys	Val	Leu	Ala	Lys	Lys	Glu	Leu	Ala	Tyr	Val	Pro	Ile	Ile	Gly	Trp							
															120			125		130		
atg tgg tac ttc acc gag atg gtc ttc tgt tgg cgc aag tgg gag cag 607																						
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															135			140		145		150
gat cgc aag acg gtt gcc acc agt ttg cag cac ctc cgg gac tac ccc 655																						
Asp	Arg	Lys	Thr	Val	Ala	Thr	Ser	Leu	Gln	His	Leu	Arg	Asp	Tyr	Pro							
															155			160		165		

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Glu Lys Tyr Phe Phe Leu Ile His Cys Glu Gly Thr Arg Phe Thr Glu	
170 175 180	
aag aag cat gag atc agc atg cag gtg gcc cgg gcc aag ggg ctg cct	751
Lys Lys His Glu Ile Ser Met Gln Val Ala Arg Ala Lys Gly Leu Pro	
185 190 195	
cgc ctc aag cat cac ctg ttg cca cga acc aag ggc ttc gcc atc acc	799
Arg Leu Lys His His Leu Leu Pro Arg Thr Lys Gly Phe Ala Ile Thr	
200 205 210	
gtg agg agc ttg aga aat gta gtt tca gct gta tat gac tgt aca ctc	847
Val Arg Ser Leu Arg Asn Val Val Ser Ala Val Tyr Asp Cys Thr Leu	
215 220 225 230	
aat ttc aga aat aat gaa aat cca aca ctg ctg gga gtc cta aac gga	895
Asn Phe Arg Asn Asn Glu Asn Pro Thr Leu Leu Gly Val Leu Asn Gly	
235 240 245	
aag aaa tac cat gca gat ttg tat gtt agg agg atc cca ctg gaa gac	943
Lys Lys Tyr His Ala Asp Leu Tyr Val Arg Arg Ile Pro Leu Glu Asp	
250 255 260	
atc cct gaa gac gat gac gag tgc tgc gcc tgg ctg cac aag ctc tac	991
Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala Trp Leu His Lys Leu Tyr	
265 270 275	
cag gag aag gat gcc ttt cag gag gag tac tac agg acg ggc acc ttc	1039
Gln Glu Lys Asp Ala Phe Gln Glu Glu Tyr Tyr Arg Thr Gly Thr Phe	
280 285 290	
cca gag acg ccc atg gtg ccc ccc cgg cgg ccc tgg acc ctc gtg aac	1087
Pro Glu Thr Pro Met Val Pro Pro Arg Arg Pro Trp Thr Leu Val Asn	
295 300 305 310	
tgg ctg ttt tgg gcc tgc ctg gtg ctc tac cct ttc ttc cag ttc ctg	1135
Trp Leu Phe Trp Ala Ser Leu Val Leu Tyr Pro Phe Phe Gln Phe Leu	
315 320 325	
gtc agc atg atc agg agc ggg tct tcc ctg acg ctg gcc agc ttc atc	1183
Val Ser Met Ile Arg Ser Gly Ser Ser Leu Thr Leu Ala Ser Phe Ile	
330 335 340	
ctc gtc ttc ttt gtg gcc tcc gtg gga gtt cga tgg atg att ggt gtg	1231
Leu Val Phe Phe Val Ala Ser Val Gly Val Arg Trp Met Ile Gly Val	
345 350 355	
acg gaa att gac aag ggc tct gcc tac ggc aac tct gac agc aag cag	1279
Thr Glu Ile Asp Lys Gly Ser Ala Tyr Gly Asn Ser Asp Ser Lys Gln	
360 365 370	
aaa ctg aat gac tgactcaggg aggtgtcacc atccgaaggg aaccttgggg	1331
Lys Leu Asn Asp	
375	
aactggtggc ctctgcatat cctccttagt gggacacggt gacaaaggct ggggtgagccc	1391



ctgctgggca cggcggaagt cacgacctct ccagccaggg agtctggtct caaggccgga 1451  
 tggggaggaa gatgttttgt aatctttttt tccccatgtg ctttagtggg ctttggtttt 1511  
 ctttttgtgc gagtgtgtgt gagaatggct gtgtggtgag tgtgaacttt gttctgtgat 1571  
 catagaaagg gtatttttagg ctgcagggga gggcagggct ggggaccgaa ggggacaagt 1631  
 tcccccttca tcttttggtg ctgagttttc tgtaaccctt gggtgccaga gataaagtga 1691  
 aaagtgcctt aggtgagatg actaaattat gcctccaaga aaaaaaaatt aaagtgcctt 1751  
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<210> 17

<211> 378

<212> PRT

<213> Homo sapiens

<400> 17

Met	Asp	Leu	Ala	Gly	Leu	Leu	Lys	Ser	Gln	Phe	Leu	Cys	His	Leu	Val
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Phe	Cys	Tyr	Val	Phe	Ile	Ala	Ser	Gly	Leu	Ile	Ile	Asn	Thr	Ile	Gln
			20					25					30		
Leu	Phe	Thr	Leu	Leu	Leu	Trp	Pro	Ile	Asn	Lys	Gln	Leu	Phe	Arg	Lys
		35					40					45			
Ile	Asn	Cys	Arg	Leu	Ser	Tyr	Cys	Ile	Ser	Ser	Gln	Leu	Val	Met	Leu
	50					55					60				
Leu	Glu	Trp	Trp	Ser	Gly	Thr	Glu	Cys	Thr	Ile	Phe	Thr	Asp	Pro	Arg
65					70					75				80	
Ala	Tyr	Leu	Lys	Tyr	Gly	Lys	Glu	Asn	Ala	Ile	Val	Val	Leu	Asn	His
			85					90						95	
Lys	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	Trp	Ser	Leu	Ser	Glu	Arg	Phe
		100						105					110		
Gly	Leu	Leu	Gly	Gly	Ser	Lys	Val	Leu	Ala	Lys	Lys	Glu	Leu	Ala	Tyr
	115					120						125			
Val	Pro	Ile	Ile	Gly	Trp	Met	Trp	Tyr	Phe	Thr	Glu	Met	Val	Phe	Cys
	130					135					140				
Ser	Arg	Lys	Trp	Glu	Gln	Asp	Arg	Lys	Thr	Val	Ala	Thr	Ser	Leu	Gln
145				150						155				160	
His	Leu	Arg	Asp	Tyr	Pro	Glu	Lys	Tyr	Phe	Phe	Leu	Ile	His	Cys	Glu
			165						170					175	
Gly	Thr	Arg	Phe	Thr	Glu	Lys	Lys	His	Glu	Ile	Ser	Met	Gln	Val	Ala
		180						185					190		

Arg Ala Lys Gly Leu Pro Arg Leu Lys His His Leu Leu Pro Arg Thr  
 195 200 205  
 Lys Gly Phe Ala Ile Thr Val Arg Ser Leu Arg Asn Val Val Ser Ala  
 210 215 220  
 Val Tyr Asp Cys Thr Leu Asn Phe Arg Asn Asn Glu Asn Pro Thr Leu  
 225 230 235 240  
 Leu Gly Val Leu Asn Gly Lys Lys Tyr His Ala Asp Leu Tyr Val Arg  
 245 250 255  
 Arg Ile Pro Leu Glu Asp Ile Pro Glu Asp Asp Asp Glu Cys Ser Ala  
 260 265 270  
 Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Phe Gln Glu Glu Tyr  
 275 280 285  
 Tyr Arg Thr Gly Thr Phe Pro Glu Thr Pro Met Val Pro Pro Arg Arg  
 290 295 300  
 Pro Trp Thr Leu Val Asn Trp Leu Phe Trp Ala Ser Leu Val Leu Tyr  
 305 310 315 320  
 Pro Phe Phe Gln Phe Leu Val Ser Met Ile Arg Ser Gly Ser Ser Leu  
 325 330 335  
 Thr Leu Ala Ser Phe Ile Leu Val Phe Phe Val Ala Ser Val Gly Val  
 340 345 350  
 Arg Trp Met Ile Gly Val Thr Glu Ile Asp Lys Gly Ser Ala Tyr Gly  
 355 360 365  
 Asn Ser Asp Ser Lys Gln Lys Leu Asn Asp  
 370 375

<210> 18  
 <211> 52  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 18  
 Pro Phe Lys Lys Gly Ala Phe His Leu Ala Gln Gln Gly Lys Ile Pro  
 1 5 10 15  
 Ile Val Pro Val Val Val Ser Asn Thr Ser Thr Leu Val Ser Pro Lys  
 20 25 30  
 Tyr Gly Val Phe Asn Arg Gly Cys Met Ile Val Arg Ile Leu Lys Pro  
 35 40 45  
 Ile Ser Thr Glu  
 50

<210> 19  
 <211> 52  
 <212> PRT  
 <213> Homo sapiens

<400> 19  
 Pro Ser Asn Cys Gly Ala Phe His Leu Ala Val Gln Ala Gln Val Pro  
   1                  5                  10                  15  
 Ile Val Pro Ile Val Met Ser Ser Tyr Gln Asp Phe Tyr Cys Lys Lys  
                   20                  25                  30  
 Glu Arg Arg Phe Thr Ser Gly Gln Cys Gln Val Arg Val Leu Pro Pro  
                   35                  40                  45  
 Val Pro Thr Glu  
                   50

<210> 20  
 <211> 18  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide

<400> 20  
 tgcaagatgg aaggcgcc

18

<210> 21  
 <211> 6  
 <212> PRT  
 <213> Homo sapiens

<400> 21  
 Gly Ala Phe His Leu Ala  
   1                  5

<210> 22  
 <211> 60  
 <212> PRT  
 <213> Saccharomyces cerevisiae

<400> 22  
 Gln Gln Gly Lys Ile Pro Ile Val Pro Val Val Val Ser Asn Thr Ser  
   1                  5                  10                  15  
 Thr Leu Val Ser Pro Lys Tyr Gly Val Phe Asn Arg Gly Cys Met Ile  
                   20                  25                  30  
 Val Arg Ile Leu Lys Pro Ile Ser Thr Glu Asn Leu Thr Lys Asp Lys  
                   35                  40                  45

Ile Gly Glu Phe Ala Glu Lys Val Arg Asp Gln Met  
 50 55 60

<210> 23  
 <211> 60  
 <212> PRT  
 <213> Homo sapiens

<400> 23  
 Val Arg Glu Asn Val Pro Ile Val Pro Val Val Tyr Ser Ser Phe Ser  
 1 5 10 15  
 Ser Phe Tyr Asn Thr Lys Lys Lys Phe Phe Thr Ser Gly Thr Val Thr  
 20 25 30  
 Val Gln Val Leu Glu Ala Ile Pro Thr Ser Gly Leu Thr Ala Ala Asp  
 35 40 45  
 Val Pro Ala Leu Arg Gly Thr Pro Ala Thr Gly Pro  
 50 55 60

<210> 24  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 24  
 cctcaaagtg tggatctatc

20

<210> 25  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide

<400> 25  
 ggaagagtac accacgggga c

21

<210> 26  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 26  
gactctagcc taggcttttg c

21

<210> 27  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 27  
ctagcttata atacgactca c

21

<210> 28  
<211> 23  
<212> PRT  
<213> Zea mays

<400> 28  
Gly Leu Gln Arg Leu Lys Asp Phe Pro Arg Pro Phe Trp Leu Ala Leu  
1 5 10 15  
Phe Val Glu Gly Thr Arg Phe  
20

<210> 29  
<211> 23  
<212> PRT  
<213> Homo sapiens

<400> 29  
Gly Leu Arg Arg Leu Ser Asp Tyr Pro Glu Tyr Met Trp Phe Leu Leu  
1 5 10 15  
Tyr Cys Glu Gly Thr Arg Phe  
20

<210> 30  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 30  
gactaccccg agtacatgtg gtttctc

27

<210> 31  
<211> 9

<212> PRT

<213> Homo sapiens

<400> 31

Asp Tyr Pro Glu Tyr Met Trp Phe Leu  
1 5

<210> 32

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 32

cacatgtccg cctcgtactt cttc

24

<210> 33

<211> 46

<212> PRT

<213> Homo sapiens

<400> 33

Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu Leu  
1 5 10 15

Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe Val Gln  
20 25 30

Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu Tyr  
35 40 45

<210> 34

<211> 46

<212> PRT

<213> Homo sapiens

<400> 34

Met Asp Leu Ala Gly Leu Leu Lys Ser Gln Phe Leu Cys His Leu Val  
1 5 10 15

Phe Cys Tyr Val Phe Ile Ala Ser Gly Leu Ile Ile Asn Thr Ile Gln  
20 25 30

Leu Phe Thr Leu Leu Leu Trp Pro Ile Asn Lys Gln Leu Phe  
35 40 45

<210> 35

<211> 29

<212> DNA

<213> Artificial Sequence

<220>  
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<400> 35  
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<210> 36  
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<212> DNA  
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<400> 36  
cctcacgcat gcaccatggg aatagc. 26

<210> 37  
<211> 24  
<212> DNA  
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<220>  
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<400> 37  
ggcgcacgac tgaggctccg gtgc 24

<210> 38  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 38  
gtagttttca cggtagcctga aatggaag 28

<210> 39  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 39  
ggcccgggtac catgggcctg ctggccttcc 30

<210> 40  
<211> 33

<212> DNA  
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<220>  
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<400> 40  
 taactcctcg agttattcct ttttcttaaa ctc 33

<210> 41  
 <211> 35  
 <212> DNA  
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<220>  
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<400> 41  
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<210> 42  
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 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 42  
 ggaggatatc tagaggccac cagttc 26

<210> 43  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<400> 43  
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 1 5

<210> 44  
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 <212> DNA  
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<220>  
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 oligonucleotide



<400> 44  
cacatgtccg cctcgtactt cttc

24

<210> 45  
<211> 21  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 45  
gactctagcc taggcttttg c

21